

SEQUENCE LISTING

<110> Wicher, Kryzysztow B.
 Holst, Olof Peder
 Hachem, Maher Youssef Abou
 Karlsson, Eva Margareta Nordberg
 Hreggvidsson, Gudmundur O.

<120> Thermostable Cellulase

<130> P5099PC00

<150> PCT/IS01/00012

<151> 2001-06-15

<150> 09/594,884

<151> 2000-06-15

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<170> FastSEQ for Windows Version 4.0

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<212> DNA

<213> Rhodothermus marinus

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cctccggcgc gacaacgtga agtggcgagc gcctggcctc tgggcgctgg ccaacgacta      300
cggcttcggg gatgtggtct actccggtcc catctacgaa cgcattggaac gtgaggatgg      360
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cggcggcgag ttcgtgattg cgggaccgga ccgtgtcttc caccggcgc gggtagcggg      480
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cttccgcacc gacgactggc cggaaggcga ctgagcgacg caaccgggtg ttgcatgcga      660
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Met Asn Val

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gag	ccg	acc	gtc	gag	ctg	tgc	gga	cgc	tgg	gac	gcg	cgc	gat	gtg	gcc	862
Glu	Pro	Thr	Val	Glu	Leu	Cys	Gly	Arg	Trp	Asp	Ala	Arg	Asp	Val	Ala	
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Gln	Cys	Ile	Glu	Val	Gly	Leu	Glu	Thr	Gly	Asn	Phe	Thr	Ile	Thr	Arg	
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Ser	Glu	Leu	Asp	Leu	Lys	Ala	Phe	Ile	Asp	Asp	Ala	Val	Ala	Arg	Gly	
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 Val Gln
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tcggggcgct tatgcgggcg gccgtcgctt tgtgcctgac tttgtagtgc gctacggagg 1595

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<212> PRT

<213> Rhodothermus marinus

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Asp Val Ala Gly Gly Arg Tyr Arg Val Ile Asn Asn Val Trp Gly Ala
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Glu Thr Ala Gln Cys Ile Glu Val Gly Leu Glu Thr Gly Asn Phe Thr
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Ala Ile Tyr Phe Gly Cys His Trp Gly Ala Cys Thr Ser Asn Ser Gly
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Leu Pro Arg Arg Val Gln Glu Leu Ser Asp Val Arg Thr Ser Trp Thr
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Leu Thr Pro Ile Thr Thr Gly Arg Trp Asn Ala Ala Tyr Asp Ile Trp
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Phe Ser Pro Val Thr Asn Ser Gly Asn Gly Tyr Ser Gly Gly Ala Glu
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Leu Met Ile Trp Leu Asn Trp Asn Gly Gly Val Met Pro Gly Gly Ser
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Arg Val Ala Thr Val Glu Leu Ala Gly Ala Thr Trp Glu Val Trp Tyr
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Ala Asp Trp Asp Trp Asn Tyr Ile Ala Tyr Arg Arg Thr Thr Pro Thr
 195 200 205

Thr Ser Val Ser Glu Leu Asp Leu Lys Ala Phe Ile Asp Asp Ala Val
 210 215 220

Ala Arg Gly Tyr Ile Arg Pro Glu Trp Tyr Leu His Ala Val Glu Thr
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gtatggggcg cggagaccgc ccagtgcatt gaggtcggac tggaaacggg caacttcacg 240

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Ile Leu Thr Ile Leu Leu Val Gln Ala Ile Tyr Phe Val Glu Lys Tyr
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cat acc tct gag gac aag tca act tca aat acc tca tct aca cca ccc 207
His Thr Ser Glu Asp Lys Ser Thr Ser Asn Thr Ser Ser Thr Pro Pro
30 35 40
caa aca aca ctt tcc act acc aag gtt ctc aag att aga tac cct gat 255
Gln Thr Thr Leu Ser Thr Thr Lys Val Leu Lys Ile Arg Tyr Pro Asp
45 50 55
gac ggt gag tgg cca gga gct cct att gat aag gat ggt gat ggg aac 303
Asp Gly Glu Trp Pro Gly Ala Pro Ile Asp Lys Asp Gly Asp Gly Asn
60 65 70
cca gaa ttc tac att gaa ata aac cta tgg aac att ctt aat gct act 351
Pro Glu Phe Tyr Ile Glu Ile Asn Leu Trp Asn Ile Leu Asn Ala Thr
75 80 85 90
gga ttt gct gag atg acg tac aat tta acc agc ggc gtc ctt cac tac 399
Gly Phe Ala Glu Met Thr Tyr Asn Leu Thr Ser Gly Val Leu His Tyr
95 100 105
gtc caa caa ctt gac aac att gtc ttg agg gat aga agt aat tgg gtg 447
Val Gln Gln Leu Asp Asn Ile Val Leu Arg Asp Arg Ser Asn Trp Val
110 115 120
cat gga tac ccc gaa ata ttc tat gga aac aag cca tgg aat gca aac 495
His Gly Tyr Pro Glu Ile Phe Tyr Gly Asn Lys Pro Trp Asn Ala Asn
125 130 135

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Tyr Ala Thr Asp Gly Pro Ile Pro Leu Pro Ser Lys Val Ser Asn Leu	
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Thr Asp Phe Tyr Leu Thr Ile Ser Tyr Lys Leu Glu Pro Lys Asn Gly	
155 160 165 170	
ctg cca att aac ttc gca ata gaa tcc tgg tta acg aga gaa gct tgg	639
Leu Pro Ile Asn Phe Ala Ile Glu Ser Trp Leu Thr Arg Glu Ala Trp	
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aga aca aca gga att aac agc gat gag caa gaa gta atg ata tgg att	687
Arg Thr Thr Gly Ile Asn Ser Asp Glu Gln Glu Val Met Ile Trp Ile	
190 195 200	
tac tat gac gga tta caa ccg gct ggc tcc aaa gtt aag gag att gta	735
Tyr Tyr Asp Gly Leu Gln Pro Ala Gly Ser Lys Val Lys Glu Ile Val	
205 210 215	
gtc cca ata ata gtt aac gga aca cca gta aat gct aca ttt gaa gta	783
Val Pro Ile Ile Val Asn Gly Thr Pro Val Asn Ala Thr Phe Glu Val	
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tgg aag gca aac att ggt tgg gag tat gtt gca ttt aga ata aag acc	831
Trp Lys Ala Asn Ile Gly Trp Glu Tyr Val Ala Phe Arg Ile Lys Thr	
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cca atc aaa gag gga aca gtg aca att cca tac gga gca ttt ata agt	879
Pro Ile Lys Glu Gly Thr Val Thr Ile Pro Tyr Gly Ala Phe Ile Ser	
255 260 265	
gtt gca gcc aac att tca agc tta cca aat tac aca gaa ctt tac tta	927
Val Ala Ala Asn Ile Ser Ser Leu Pro Asn Tyr Thr Glu Leu Tyr Leu	
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Glu Asp Val Glu Ile Gly Thr Glu Phe Gly Thr Pro Ser Thr Thr Ser	
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Ala His Leu Glu Trp Trp Ile Thr Asn Ile Thr Leu Thr Pro Leu Asp	
300 305 310	
aga cct ctt att tcc taa atttcggcaa cctgggaatt atcaagttta	1071
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 35 40 45

Thr Lys Val Leu Lys Ile Arg Tyr Pro Asp Asp Gly Glu Trp Pro Gly
 50 55 60

Ala Pro Ile Asp Lys Asp Gly Asp Gly Asn Pro Glu Phe Tyr Ile Glu
 65 70 75 80

Ile Asn Leu Trp Asn Ile Leu Asn Ala Thr Gly Phe Ala Glu Met Thr
 85 90 95

Tyr Asn Leu Thr Ser Gly Val Leu His Tyr Val Gln Gln Leu Asp Asn
 100 105 110

Ile Val Leu Arg Asp Arg Ser Asn Trp Val His Gly Tyr Pro Glu Ile
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Phe Tyr Gly Asn Lys Pro Trp Asn Ala Asn Tyr Ala Thr Asp Gly Pro
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Ile Ser Tyr Lys Leu Glu Pro Lys Asn Gly Leu Pro Ile Asn Phe Ala
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Ile Glu Ser Trp Leu Thr Arg Glu Ala Trp Arg Thr Thr Gly Ile Asn
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Ser Asp Glu Gln Glu Val Met Ile Trp Ile Tyr Tyr Asp Gly Leu Gln
 195 200 205

Pro Ala Gly Ser Lys Val Lys Glu Ile Val Val Pro Ile Ile Val Asn
 210 215 220

Gly Thr Pro Val Asn Ala Thr Phe Glu Val Trp Lys Ala Asn Ile Gly
 225 230 235 240

Trp Glu Tyr Val Ala Phe Arg Ile Lys Thr Pro Ile Lys Glu Gly Thr
 245 250 255

Val Thr Ile Pro Tyr Gly Ala Phe Ile Ser Val Ala Ala Asn Ile Ser
 260 265 270

Ser Leu Pro Asn Tyr Thr Glu Leu Tyr Leu Glu Asp Val Glu Ile Gly
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